

**inuits**  
OPEN SOURCE INNOVATORS

# Don't Panic! Mostly Harmless Docs on Creating Easyconfigs

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*Denis Kristak  
(deniskristak)  
Orient Kruzik  
(ItIsl-Orient)*



Who is Inuits?



We bring **Open Source** to companies and governments to build **innovative solutions**

8  
igloos

4  
Countries

180+  
Employees



# OUR SERVICES



Technology  
solutions



Business  
Solutions



Research &  
Development

# Technology solutions

**Continuous Delivery  
& Continuous Deployments**

**Infrastructure as  
Code**

**Monitoring and  
Observability**

**Container  
Orchestration**

# Business solutions





Inuits @ EasyBuild

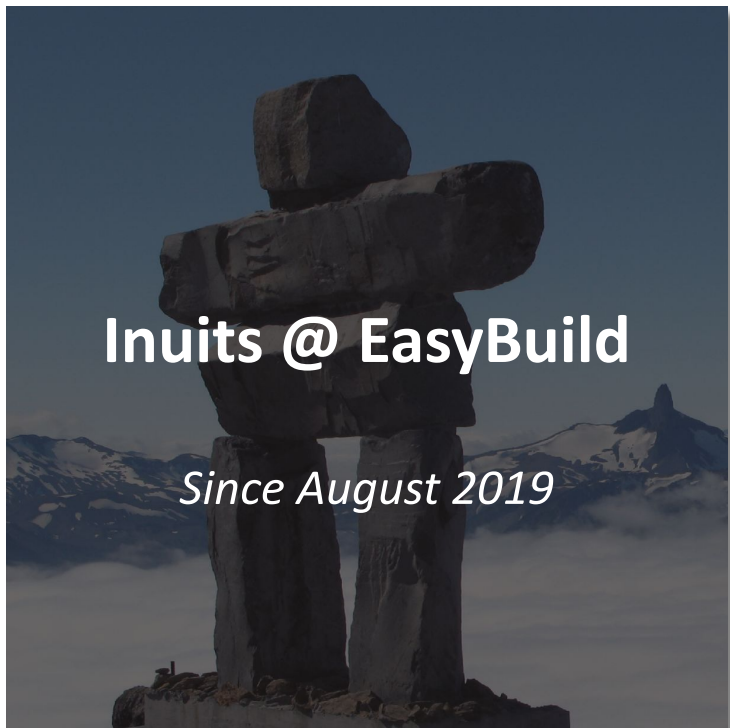
- Contributing to Open Source while getting paid
- What?
  - Easyconfigs, mostly
- Why?
  - Works on my machine approach :-)



```

... .. @@ -0,0 +1,84 @@
1 + adding option to the run_finder script, to be able to run without using singularity or docker
2 + author: Denis Kristak (INUITIS)
3 + diff -ruN Finder-finder_v1.1.0_orig/run_finder Finder-finder_v1.1.0/run_finder
4 + --- Finder-finder_v1.1.0_orig/run_finder      2021-12-19 20:46:57.000000000 +0100
5 + +++ Finder-finder_v1.1.0/run_finder          2022-12-15 12:08:39.120630477 +0100
6 + @@ -45,7 +45,7 @@
7 +     optional_named.add_argument( "--skip_cpd", "--skip_cpd", help = "Turn on this option to skip changepoint detection. Could be effective for grasses", action =
8 + "store_true" )
9 +     optional_named.add_argument( "--exonerate_gff3", "-egff3", help = "Enter the exonerate output in gff3 format" )
10 +     optional_named.add_argument( "--star_shared_mem", "--star_shared_mem", help = "Turn on this option if you want STAR to load the genome index into shared
11 + memory. This saves memory if multiple finder runs are executing on the same host, but might not work in your cluster environment.", action = "store_true" )
12 +     optional_named.add_argument( "--framework", "-fm", help = "Enter your choice of framework", choices = ["docker", "singularity"], default = "docker" )
13 +     optional_named.add_argument( "--framework", "-fm", help = "Enter your choice of framework", choices = ["docker", "singularity", "bare"], default = "bare" )
14 +
15 +     # optional_named.add_argument("--intron_gff3","-intron_gff3",help="Enter the name and location of the file containing introns in gff3 format")
16 +     # optional_named.add_argument("--ground_truth_gtf","-gt_gtf",help="Enter the gtf filename of the actual annotation [for developmental purposes]")
17 + @@ -86,6 +86,12 @@
18 +     singularity_cmd += f" bash -c {command}"
19 +     os.system( singularity_cmd )
20 +
21 + +def runBareCommand( command ):
22 + +    """
23 + +    Runs the command directly on the system
24 + +    """
25 + +    # Runs the main command
26 + +    os.system( command )
27 +
28 + def main():
29 +     commandLineArg = sys.argv
30 +
31 +     @@ -98,8 +104,8 @@
32 +
33 +         f"{ '/' .join(options.genome.split('/')[:-1])}:{ '/' .join(options.genome.split('/')[:-1]) }",
34 +         f"{options.output_directory}:{options.output_directory}"
35 +
36 +

```



461

**Easyconfigs**

8

**Easyblocks**

FW

**Easystack development**



Docs (or DIY)

## The Problem



**A lot of <3 for EasyBuild & UGent**



**A lot of requests for supported software**



**People can wait months for new EC**

## The Solution



**Good step-by-step documentation**



**People can easily write Easyconfigs**



**You win & we win & community wins**





Example



Homepage: <https://multiqc.info/>  
Github: <https://github.com/ewels/MultiQC>

master 10 branches 27 tags

Go to file

Add file

Code

## About

Aggregate results from bioinformatics analyses across many samples into a single report.

[multiqc.info](#)[python](#) [bioinformatics](#) [analysis](#)  
[pypi](#) [bioconda](#) [multiqc](#)[Readme](#)[GPL-3.0 license](#)[Cite this repository](#)

987 stars

40 watching

528 forks

Report repository





















## Releases 27

[MultiQC Version 1.14](#) Latest  
on Jan 8[+ 26 releases](#)

## Packages 1

[multiqc](#)

Used by 254

 ewels	Remove docs-restructure branch from docs preview workflow	623e9a1 3 weeks ago	5,703 commits
 .github	Remove docs-restructure branch from docs preview workflow		3 weeks ago
 docs	Merge branch 'master' into docs-restructure		3 weeks ago
 multiqc	Porechop: No barplots if no data.		2 months ago
 test	Remove py2 'from __future__ import print_function'		7 months ago
 .dockerignore	Added git and python things to docker ignore		last year
 .gitignore	Merge branch 'master' into cellranger-module		4 months ago
 .gitmodules	Added test data back as a submodule. Now stored in MultiQC_TestD...		8 years ago
 .markdownlint.yaml	Add and fix markdownlint		3 years ago
 .pre-commit-config.yaml	Remove unused Python imports		3 months ago
 .prettierrc	Prettier: CSS and JavaScript		3 years ago
 .prettierrc.yaml	Prettier: CSS and JavaScript		3 years ago
 CHANGELOG.md	Sort changelog modules		2 months ago
 CITATION.cff	Run prettier		10 months ago
 CSP.txt	Add new CSP for the new javascript file		4 months ago
 Dockerfile	Run multiqc --help at the end of the dockerfile to check build is good		3 months ago
 LICENSE	Changed licence from MIT to GNU GPLv3		7 years ago
 MANIFEST.in	Cleaned manifest, set version number to devel.		8 years ago
 README.md	New logos! MultiQC is now developed and maintained at Seqera La...		3 months ago
 flake.lock	Added nix flake support		9 months ago

```
50     zip_safe=False,  
51     install_requires=[  
52         "matplotlib>=2.1.1",  
53         "networkx>=2.5.1",  
54         "numpy",  
55         "click",  
56         "coloredlogs",  
57         "future>0.14.0",  
58         "jinja2>=3.0.0",  
59         "lzstring",  
60         "markdown",  
61         "pyyaml>=4",  
62         "requests",  
63         "rich>=10",  
64         "rich-click",  
65         "simplejson",  
66         "spectra>=0.0.10",  
67     ],
```

```
easyblock = 'PythonBundle'

name = 'MultiQC'
version = '1.12'

homepage = 'https://multiqc.info'
description = """Aggregate results from bioinformatics analyses across many samples into a single report.

MultiQC searches a given directory for analysis logs and compiles an HTML report. It's a general
use tool, perfect for summarising the output from numerous bioinformatics tools."""

toolchain = {'name': 'foss', 'version': '2021b'}
```



```
easyblock = 'PythonBundle'

name = 'MultiQC'
version = '1.14'

homepage = 'https://multiqc.info'
description = """Aggregate results from bioinformatics analyses across many samples into a single report.

MultiQC searches a given directory for analysis logs and compiles an HTML report. It's a general
use tool, perfect for summarising the output from numerous bioinformatics tools."""

toolchain = {'name': 'foss', 'version': '2022a'}
```

```
dependencies = [  
    ('Python', '3.9.6'),  
    ('matplotlib', '3.4.3'),  
    ('PyYAML', '5.4.1'),  
    ('networkx', '2.6.3'),  
]  
  
use_pip = True  
  
exts_list = [  
    ('colormath', '3.0.0', {  
        'checksums': ['3d4605af344527da0e4f9f504fad7ddbcbda35322c566a6c72e28edb1ff31217'],  
    }  
),  
    ('spectra', '0.0.11', {  
        'checksums': ['8eb362a5187cb63cee13cd01186799c0c791a3ad3bec57b279132e12521762b8'],  
    }  
),  
    ('Markdown', '3.2.1', {  
        'checksums': ['90fee683eeabe1a92e149f7ba74e5ccdc81cd397bd6c516d93a8da0ef90b6902'],  
    }  
),  
    ('lzstring', '1.0.4', {  
        'checksums': ['1afa61e598193fbcc211e0899f09a9679e33f9102bcc37fbfda0b7fef4d9ea2'],  
    }  
),  
    ('coloredlogs', '15.0.1', {  
        'checksums': ['7c991aa71a4577af2f82600d8f8f3a89f936baeaf9b50a9c197da014e5bf16b0'],  
    }  
),  
    ('rich', '10.16.0', {  
        'checksums': ['06a1355131feda5eba4511dd749e9187ac0fb42209e189845d81e94505fc268e'],  
    }  
),  
    ('commonmark', '0.9.1', {  
        'checksums': ['452f9dc859be7f06631ddcb328b6919c67984aca654e5fefb3914d54691aed60'],  
    }  
),  
    ('humanfriendly', '10.0', {  
        'checksums': ['6b0b831ce8f15f7300721aa49829fc4e83921a9a301cc7f606be6686a2288ddc'],  
    }  
),  
    ('multiqc', version, {  
        'checksums': ['c62a8d24e3d1cebb42b615ac48201ecf4f2f863772f8f9fa59e466753d4af531'],  
    }  
),  
]
```

<code>foss</code>	<i>date</i>	<i>binutils</i>	<i>GCC</i>	<i>Open MPI</i>	<i>FlexiBLAS</i>	<i>OpenBLAS</i>	<i>LAPACK</i>	<i>ScaLAPACK</i>	<i>FFTW</i>
2019a	Jan '19	2.31.1	8.2.0	3.1.3	<i>(none)</i>	0.3.5	(incl. with OpenBLAS)	2.0.2	3.3.8
2019b	Sept '19	2.32	8.3.0	3.1.4	<i>(none)</i>	0.3.7	(incl. with OpenBLAS)	2.0.2	3.3.8
2020a	May '20	2.34	9.3.0	4.0.3	<i>(none)</i>	0.3.9	(incl. with OpenBLAS)	2.1.0	3.3.8
2020b	Nov '20	2.35	10.2.0	4.0.5	<i>(none)</i>	0.3.12	(incl. with OpenBLAS)	2.1.0	3.3.8
2021a	May '21	2.36.1	10.3.0	4.1.1	3.0.4	0.3.15	(incl. with OpenBLAS)	2.1.0	3.3.9
2021b	Oct '21	2.37	11.2.0	4.1.1	3.0.4	0.3.18	(incl. with OpenBLAS)	2.1.0	3.3.10
2022a	Jun '22	2.38	11.3.0	4.1.4	3.2.0	0.3.20	(incl. with OpenBLAS)	2.2.0	3.3.10
2022b	Dec '22	2.39	12.2.0	4.1.4	3.2.1	0.3.21	(incl. with OpenBLAS)	2.2.0	3.3.10

```
$ eb -S ^Python-\\d
CFGS1=/user/gent/445/vsc44588/easybuild/easybuild-easyconfigs/easybuild/easyconfigs
* $CFGS1/p/Python/Python-2.5.6_svnversion-cmd.patch
* $CFGS1/p/Python/Python-2.7.9-GCC-4.8.4-bare.eb
* $CFGS1/p/Python/Python-2.7.9-GCC-4.9.2-bare.eb
* $CFGS1/p/Python/Python-2.7.10-GCC-4.9.3-2.25-bare.eb
* $CFGS1/p/Python/Python-2.7.10-GNU-4.9.3-2.25-bare.eb
[...]
* $CFGS1/p/Python/Python-3.10.4-GCCcore-11.3.0.eb
* $CFGS1/p/Python/Python-3.10.8-GCCcore-12.2.0-bare.eb
* $CFGS1/p/Python/Python-3.10.8-GCCcore-12.2.0.eb
* $CFGS1/p/Python/Python-3.11.2-GCCcore-12.2.0-bare.eb
* $CFGS1/p/Python/Python-3_9-blist-1.3.6-fix-undefined_symbol_PyObject_GC_IS_TRACKED.patch
* $CFGS1/p/Python/python-2.7.5_libffi_int128_icc.patch
* $CFGS1/p/Python/python-2.7_libffi-include-xmmintrin.patch
* $CFGS1/p/Python/python-3.3_libffi-include-xmmintrin.patch
* $CFGS1/p/Python/python-3.4_libffi-include-xmmintrin.patch
```

```
dependencies = [
    ('Python', '3.10.4'),
    ('matplotlib', '3.4.3'),
    ('PyYAML', '5.4.1'),
    ('networkx', '2.6.3'),
]

use_pip = True

exts_list = [
    ('colormath', '3.0.0', {
        'checksums': ['3d4605af344527da0e4f9f504fad7ddbcbda35322c566a6c72e28edb1ff31217'],
    }),
    ('spectra', '0.0.11', {
        'checksums': ['8eb362a5187cb63cee13cd01186799c0c791a3ad3bec57b279132e12521762b8'],
    }),
    ('Markdown', '3.2.1', {
        'checksums': ['90fee683eeabe1a92e149f7ba74e5ccdc81cd397bd6c516d93a8da0ef90b6902'],
    }),
    ('lzstring', '1.0.4', {
        'checksums': ['1afa61e598193fbcc211e0899f09a9679e33f9102bcc37fbfda0b7fef4d9ea2'],
    }),
    ('coloredlogs', '15.0.1', {
        'checksums': ['7c991aa71a4577af2f82600d8f8f3a89f936baeaf9b50a9c197da014e5bf16b0'],
    }),
    ('rich', '10.16.0', {
        'checksums': ['06a1355131feda5eba4511dd749e9187ac0fb42209e189845d81e94505fc268e'],
    }),
    ('commonmark', '0.9.1', {
        'checksums': ['452f9dc859be7f06631ddcb328b6919c67984aca654e5fefb3914d54691aed60'],
    }),
    ('humanfriendly', '10.0', {
        'checksums': ['6b0b831ce8f15f7300721aa49829fc4e83921a9a301cc7f606be6686a2288ddc'],
    }),
    ('multiqc', version, {
        'checksums': ['c62a8d24e3d1cebb42b615ac48201ecf4f2f863772f8f9fa59e466753d4af531'],
    }),
]
```



```
dependencies = [
    ('Python', '3.10.4'),
    ('matplotlib', '3.5.2'),
    ('PyYAML', '6.0'),
    ('networkx', '2.8.4'),
]

use_pip = True

exts_list = [
    ('colormath', '3.0.0', {
        'checksums': ['3d4605af344527da0e4f9f504fad7ddbcbda35322c566a6c72e28edb1ff31217'],
    }),
    ('spectra', '0.0.11', {
        'checksums': ['8eb362a5187cb63cee13cd01186799c0c791a3ad3bec57b279132e12521762b8'],
    }),
    ('Markdown', '3.4.1', {
        'checksums': ['90fee683eeabe1a92e149f7ba74e5ccdc81cd397bd6c516d93a8da0ef90b6902'],
    }),
    ('lzstring', '1.0.4', {
        'checksums': ['1afa61e598193fbcc211e0899f09a9679e33f9102bcc37fbfda0b7fef4d9ea2'],
    }),
    ('coloredlogs', '15.0.1', {
        'checksums': ['7c991aa71a4577af2f82600d8f8f3a89f936baeaf9b50a9c197da014e5bf16b0'],
    }),
    ('rich', '13.3.1', {
        'checksums': ['06a1355131feda5eba4511dd749e9187ac0fb42209e189845d81e94505fc268e'],
    }),
    ('commonmark', '0.9.1', {
        'checksums': ['452f9dc859be7f06631ddcb328b6919c67984aca654e5fefb3914d54691aed60'],
    }),
    ('humanfriendly', '10.0', {
        'checksums': ['6b0b831ce8f15f7300721aa49829fc4e83921a9a301cc7f606be6686a228ddc'],
    }),
    ('multiqc', version, {
        'checksums': ['c62a8d24e3d1cebb42b615ac48201ecf4f2f863772f8f9fa59e466753d4af531'],
    }),
]
```

```
ERROR: Build of /kyukon/home/gent/445/vsc44588/temp/eum/MultiQC-1.12-foss-2021b.eb failed (err: 'build failed (first 300 chars): `/apps/gent/RHEL8/cascadelake-ib/software/Python/3.10.4-GCCcore-11.3.0/bin/python -m pip check` failed:\nrich 13.3.1 requires markdown-it-py, which is not installed.\nmultiqc 1.14 requires rich-click, which is not installed.\nrich 13.3.1 has requirement pygments<3.0.0,>=2.14.0, but you have pygments 2.')
```

```
exts_list = [
    ('colormath', '3.0.0', {
        'checksums': ['3d4605af344527da0e4f9f504fad7ddbebd35322c566a6c72e28edb1ff31217'],
    }),
    ('spectra', '0.0.11', {
        'checksums': ['8eb362a5187cb63cee13cd01186799c0c791a3ad3bec57b279132e12521762b8'],
    }),
    ('Markdown', '3.4.1', {
        'checksums': ['3b809086bb6efad416156e00a0da66fe47618a5d6918dd688f53f40c8e4cfeff'],
    }),
    ('lzstring', '1.0.4', {
        'checksums': ['1afa61e598193fbcc211e0899f09a9679e33f9102bcc37fbfda0b7fef4d9ea2'],
    }),
    ('coloredlogs', '15.0.1', {
        'checksums': ['7c991aa71a4577af2f82600d8f8f3a89f936baeaf9b50a9c197da014e5bf16b0'],
    }),
    ('mdurl', '0.1.2', {
        'checksums': ['bb413d29f5eea38f31dd4754dd7377d4465116fb207585f97bf925588687c1ba'],
    }),
    ('markdown-it-py', '2.1.0', {
        'checksums': ['cf7e59fed14b5ae17c0006eff14a2d9a00ed5f3a846148153899a0224e2c07da'],
        'modulename': 'markdown_it',
    }),
    ('Pygments', '2.14.0', {
        'checksums': ['b3ed06a9e8ac9a9aae5a6f5dbe78a8a58655d17b43b93c078f094ddc476ae297'],
    }),
    ('rich', '13.3.1', {
        'checksums': ['125d96d20c92b946b983d0d392b84ff945461e5a06d3867e9f9e575f8697b67f'],
    }),
    ('commonmark', '0.9.1', {
        'checksums': ['452f9dc859be7f06631ddcb328b6919c67984aca654e5fefb3914d54691aed60'],
    }),
    ('humanfriendly', '10.0', {
        'checksums': ['6b0b831ce8f15f7300721aa49829fc4e83921a9a301cc7f606be6686a2288ddc'],
    }),
    ('rich-click', '1.6.1', {
        'checksums': ['f8ff96693ec6e261d1544e9f7d9a5811c5ef5d74c8adb4978430fc0dac16777e'],
    }),
    ('multiqc', version, {
        'checksums': ['dcbba405f0c9521ed2bbd7e8f7a9200643047311c9619878b81d167300149362'],
    }),
]
```

```
sanity_check_paths = {  
    'files': ['bin/multiqc'],  
    'dirs': ['lib/python%(pyshortver)s/site-packages'],  
}  
  
sanity_check_commands = ["multiqc --help"]  
  
sanity_pip_check = True
```

```
$ eb MultiQC-1.12-foss-2021b.eb --inject-checksums
== Temporary log file in case of crash /tmp/vsc44588/eb-t7q3su5a/easybuild-mrp_sa5c.log
== injecting sha256 checksums in
/kyukon/home/.../MultiQC-1.12-foss-2021b.eb
== fetching sources & patches for MultiQC-1.12-foss-2021b.eb...
== backup of easyconfig file saved to
/kyukon/home/.../MultiQC-1.12-foss-2021b.eb.bak_202304241
24023_284525...
== injecting sha256 checksums for sources & patches in
MultiQC-1.12-foss-2021b.eb...
== injecting sha256 checksums for extensions in MultiQC-1.12-foss-2021b.eb...
== * colormath-3.0.0.tar.gz:
3d4605af344527da0e4f9f504fad7ddbcbda35322c566a6c72e28edb1ff31217
== * spectra-0.0.11.tar.gz:
8eb362a5187cb63cee13cd01186799c0c791a3ad3bec57b279132e12521762b8
== * Markdown-3.4.1.tar.gz:
3b809086bb6efad416156e00a0da66fe47618a5d6918dd688f53f40c8e4cfeff
== * lzstring-1.0.4.tar.gz:
1afa61e598193fbcc211e0899f09a9679e33f9102bcc37fbfda0b7fef4d9ea2
== * coloredlogs-15.0.1.tar.gz:
7c991aa71a4577af2f82600d8f8f3a89f936baeaf9b50a9c197da014e5bf16b0
== * rich-13.3.1.tar.gz:
125d96d20c92b946b983d0d392b84ff945461e5a06d3867e9f9e575f8697b67f
== * commonmark-0.9.1.tar.gz:
452f9dc859be7f06631ddcb328b6919c67984aca654e5fefb3914d54691aed60
== * humanfriendly-10.0.tar.gz:
6b0b831ce8f15f7300721aa49829fc4e83921a9a301cc7f606be6686a2288ddc
== * multiqc-1.14.tar.gz:
dcbba405f0c9521ed2bbd7e8f7a9200643047311c9619878b81d167300149362
```



```
$ eb --new-pr MultiQC-1.12-foss-2021b.eb
== Temporary log file in case of crash /tmp/vsc44588/eb-ustlynes/easybuild-p7deb0t9.log
== cloning git repo from /user/gent/445/vsc44588/easybuild/easybuild-easyconfigs...
== fetching branch 'develop' from https://github.com/easybuilders/easybuild-easyconfigs.git...
== copying files to /tmp/vsc44588/eb-ustlynes/git-working-dir_c6knyp_/easybuild-easyconfigs...
== pushing branch '20230424124756_new_pr_MultiQC114' to remote 'github_ItIsI-Orient_fDRrB' (git@github.com:ItIsI-Orient/easybuild-easyconfigs.git)

Opening pull request
* target: easybuilders/easybuild-easyconfigs:develop
* from: ItIsI-Orient/easybuild-easyconfigs:20230424124756_new_pr_MultiQC114
* labels: (none)
* description:
"""
(created using `eb --new-pr`)
"""
* overview of changes:
easybuild/easyconfigs/m/MultiQC/MultiQC-1.14-foss-2022a.eb | 17 ++-----
1 file changed, 2 insertions(+), 15 deletions(-)

== Temporary log file(s) /tmp/vsc44588/eb-ustlynes/easybuild-p7deb0t9.log* have been removed.
== Temporary directory /tmp/vsc44588/eb-ustlynes has been removed.
```



# inuits

OPEN SOURCE INNOVATORS

INUIITS BV

Essensteenweg 31

2930 Brasschaat

Belgium

BE 0891.514.231

**Contact:**

+32.380.821.05

[info@inuits.eu](mailto:info@inuits.eu)

[inuits.eu](http://inuits.eu)

[orient@inuits.eu](mailto:orient@inuits.eu)

[thenis@inuits.eu](mailto:thenis@inuits.eu)

or just approach us anytime ;-)